CLAIM AMENDMENTS:

Please amend the claims as indicated:

1-26. (CANCELED)

26. (CURRENTLY AMENDED) A method for eliminating redundant sequences that are common between two samples, the method comprising of the steps:

isolating RNA strands from a first sample;

isolating RNA strands from a second sample;

generating cDNA strands from the RNA strands from the first sample:

mixing the cDNA strands of the first sample with the RNA strands from the second sample;

hybridizing the cDNA strands and RNA strands with common sequences to form cDNA/RNA compliments complements, the cDNA strands and the RNA strands without common sequences remaining unhybridized cDNA strands and unhybridized RNA strands; and

degrading the cDNA/RNA eempliments complements to leave the unhybridized cDNA strands and the unhybridized RNA strands.

- 27. (PREVIOUSLY PRESENTED) The method of Claim 26, wherein the step of generating cDNA strands from the RNA strands from the first sample comprises performing RT-PCR.
- 28. (CANCELLED)
- 29. (PREVIOUSLY PRESENTED) The method of Claim 26, wherein the first sample is a healthy tissue and the second sample is a diseased tissue.
- 30. (PREVIOUSLY PRESENTED) The method of Claim 26, wherein the first sample is a diseased tissue and the second sample is a healthy tissue.
- (PREVIOUSLY PRESENTED) The method of Claim 26, further comprising: amplifying the unhybridized cDNA strands using PCR.

- (PREVIOUSLY PRESENTED) The method of Claim 26, further comprising: producing a second set of cDNA strands from the unhybridized RNA strands.
- (PREVIOUSLY PRESENTED) The method of Claim 32, further comprising: amplifying the second set of cDNA strands using PCR.
- 34. (CURRENTLY AMENDED) The method of Claim 26, wherein the step of degrading empliments complements is performed with an Exonuclease III enzyme.
- 35. (CANCELLED)
- (PREVIOUSLY PRESENTED) The method of Claim 26, further comprising: displaying at least one of the unhybridized cDNA strands and the unhybridized RNA strands.
- 37. (PREVIOUSLY PRESENTED) The method of Claim 36, wherein the step of displaying comprises using electrophoresis.
- 38. (PREVIOUSLY PRESENTED) The method of Claim 26, further comprising: reading at least one of the unhybridized cDNA strands and the unhybrized RNA strands with an autoradiogram.
- (PREVIOUSLY PRESENTED) The method of Claim 26, wherein the first and second samples are selected from the group consisting of cells, tissues, pathogens, plants, and animals.
- 40. (PREVIOUSLY PRESENTED) The method of Claim 26, wherein the first and second sample are differentiated due to a diseased state, developmental change, or induced by an external or internal stimulus.

- 41. (CURRENTLY AMENDED) A method for determining differences between a first sample of cDNA strands and a second sample of RNA strands, the method comprising of the steps:

 mixing the first sample of cDNA strands with the second sample of RNA strands;

 hybridizing the cDNA strands and the RNA strands with common sequences to form

 cDNA/RNA compliments complements, the cDNA strands and the RNA strands

 without common sequences remaining unhybridized cDNA strands and
 unhybridized RNA strands;
 - degrading the cDNA/RNA eempliments complements to leave the unhybridized cDNA strands and the unhybridized RNA strands; and
 - analyzing at least one of the unhydridized cDNA strands and the unhybridized RNA strands to determine differences between the first sample and the second sample.
- 42. (CANCELLED)
- (PREVIOUSLY PRESENTED) The method of Claim 41, further comprising: amplifying the unhybridized cDNA strands using PCR.
- (PREVIOUSLY PRESENTED) The method of Claim 41, further comprising: producing a further set of cDNA strands from the unhybridized RNA strands.
- (PREVIOUSLY PRESENTED) The method of Claim 44, further comprising: amplifying the further set of cDNA strands using PCR.
- 46. (CURRENTLY AMENDED) The method of Claim 41, wherein the step of degrading empliments complements is performed with an Exonuclease III enzyme.
- 47. (CANCELLED)